



09370406 09304013

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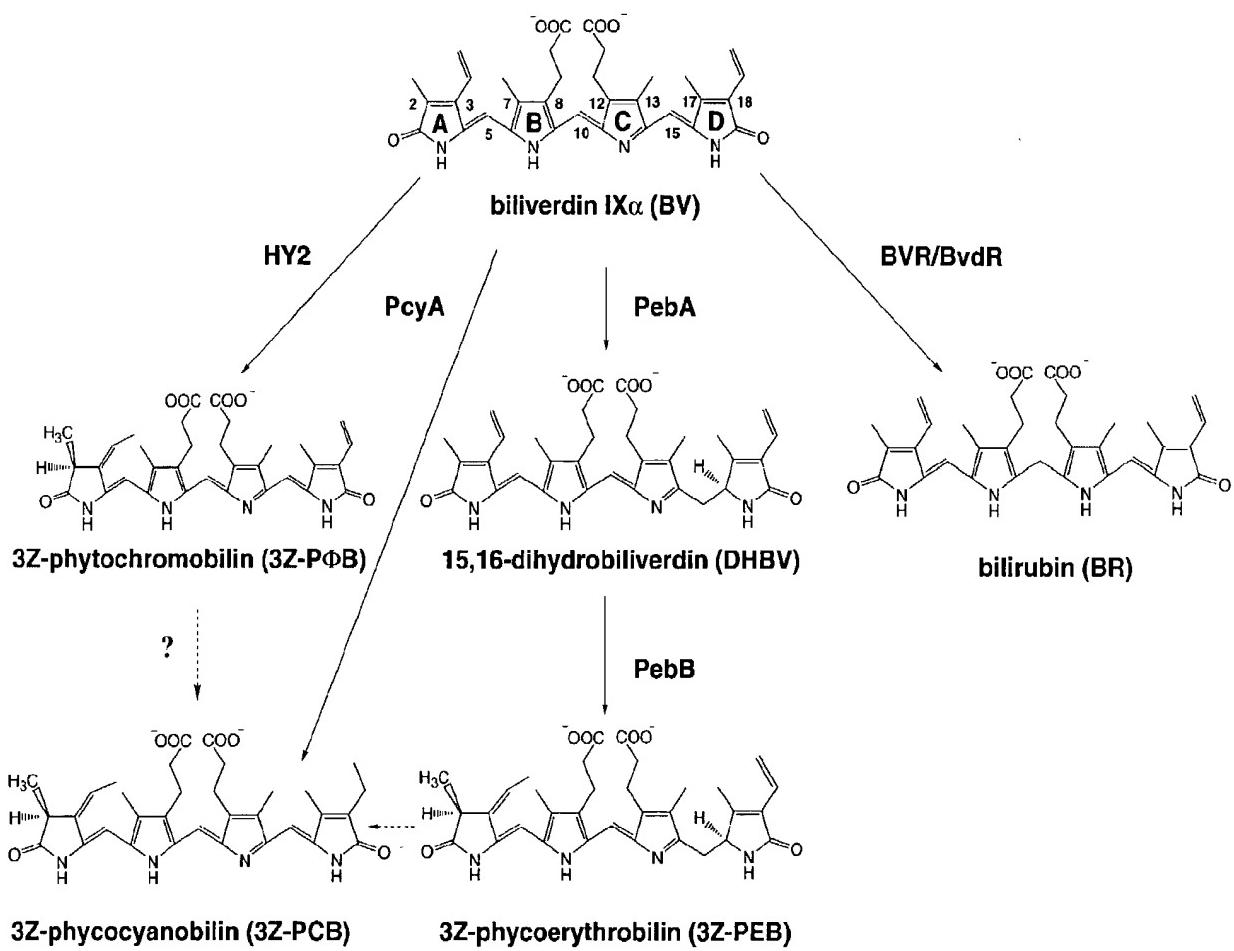


Fig. 1



03403704006 03403704006

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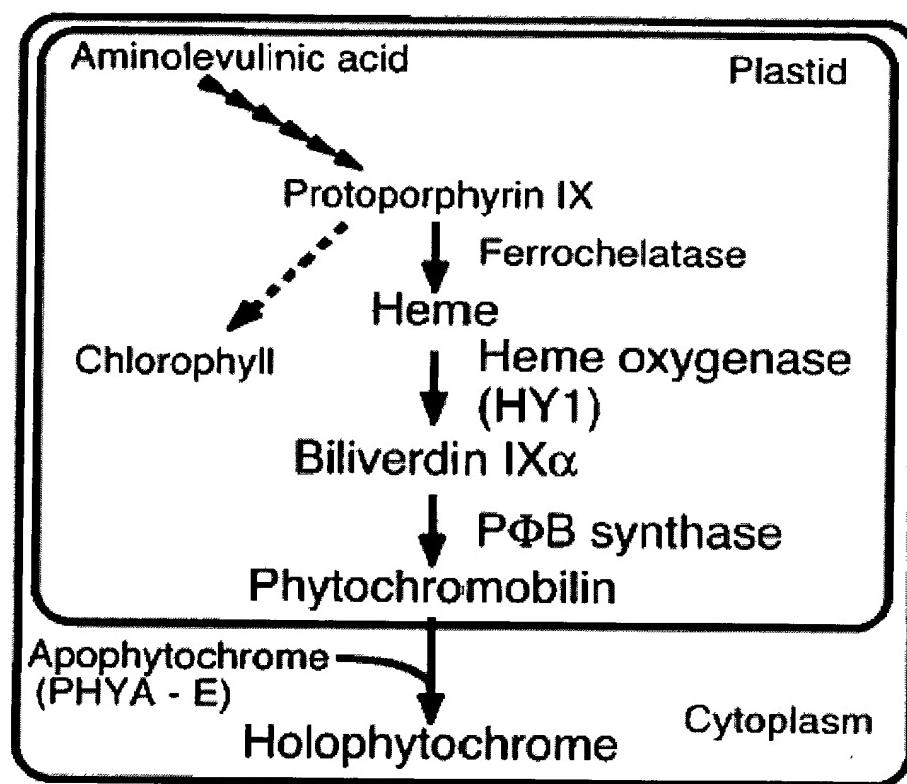


Fig. 2



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gaattccccacgtcaacgtgactgtcattcacgtggcgatgtggccctatagttgg 60
accatgactcgacggatgtgaaattcattgtcggtccaaatgcgttgtctcaactga 120
aactgtgaaaatttatctctttatagataaAGAACATCTGCTTTTCAGTTTCAGTA 180
TGAAGAAGAATTGAAGAGAGTGTCCGAGGAAGGAGACCTTGGTTTCAGTTGTGAGTCT 240
TGTTGTAATGGCTTATCAATGGAGTTGGGTTTCATTGGGTCAAGGCACC 300
M A L S M E F G F S I G S C F K A P
AAACCCACCTGTTCTAATCTCTGCAAGCCCTAATAAGATCAATTACGTTGAGAAGGAG 360
N P P V L I S A S P N K I N F T L R R R
AAAGAAAAAGATTCTTACTTAGAGTCTCTGCTGTGCGTATAAGGAATTCGCAGAGTCTGC 420
*hy2-106 ******
K X R F L L R V S A V S Y K E F A E S A
TTTAGAAGAAAACCAGGAAAAGGATCGTCTTGAACCTCACATCTCCAGgtatatgcata 480
L E E T R K R I V L E P S H L Q
tacatttcgttagtgttagtggaggattatattctcattgttcttgctgtgaattttg 540
ggtaaattgattgagttgtcattaggaaccaaacaataactttactgttataactgc 600
ttatataagtaaaagttcagattttgtttctaatcacaactgtttcagAAAAAGTA 660
E K Y
TAGTAGCATGACAGGACTAGATGGTAAGACCGAACCTCAAATGCTTGCTTTAAATCTC 720
S S M T G L D G K T E L Q M L A F K S S
AAAGATTAGACTCTGAGGAGTATGGCAATAGAGAACATGCAGgttaacttca 780
K I R L L R S M A I E N E T M Q
gcagtgacaaactgattgtttagtcccatttcatttcaattgattgattgttcta 840
*hy2-105 ******
tcttcgttagGTCTTGACTTGCAGGTTTCATGGAGCCTGAGTATGATACTCCCATAT 900
hy2-1, hy2-104 T
V F D F A G F M E P E Y D T P I F
TCTGTGCTAACTTTTACATCTACCAACGTTAACATAGTTGTATTgttaagtatcttct 960
C A N F F T S T N V N I V V L
agttatgtggagttatcaggtctgtattgtccaaactgatgttcaatatttactgtat 1020

Fig. 3B



和諧的、溫馨的、富有人情味的。

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Fig. 3B cont'd.



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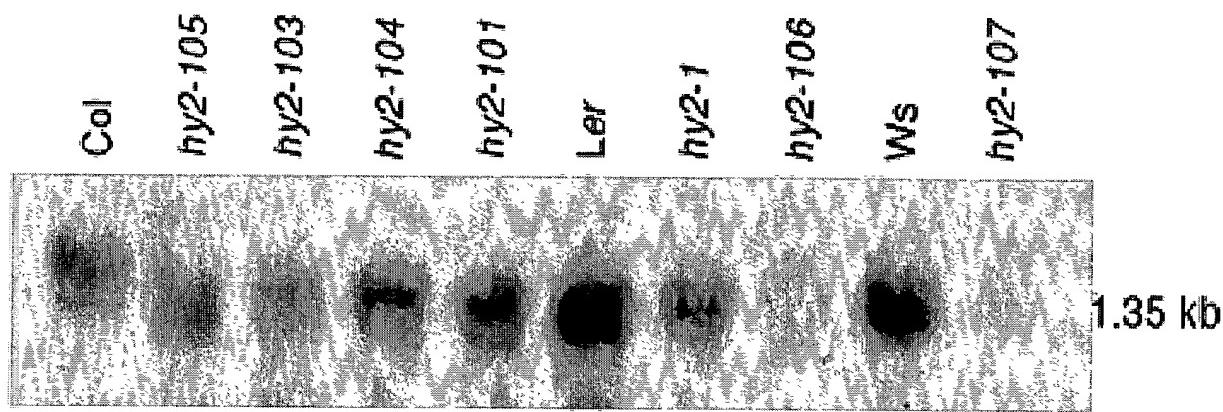


Fig. 4A

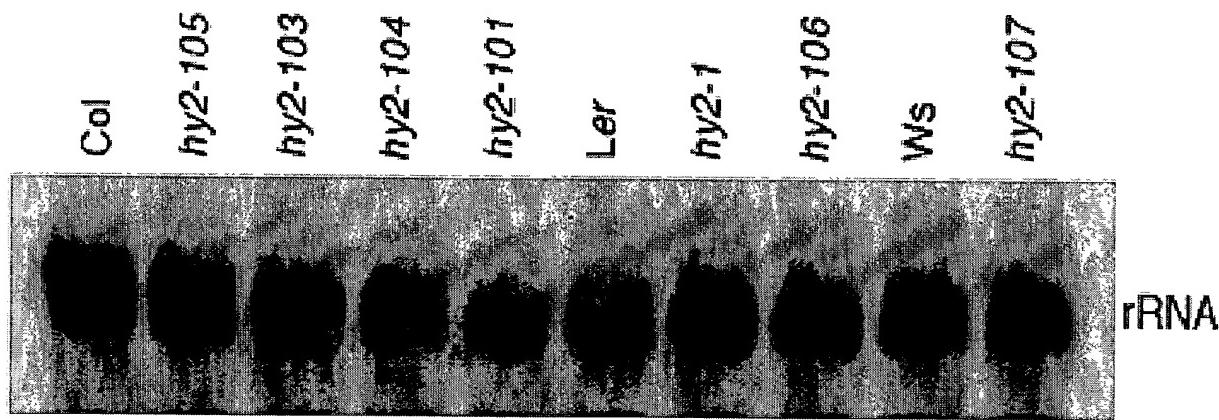


Fig. 4B



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* * * * *	20	* * * * *
HY2_ARATH	: MALSMEEFGFSIGGSCPKA PNP PVLISASPNKINFTLRRRKK	
YCP2_SYNPY	: -----	
YHP2_PROMA	: -----	
YHP3_PROMA	: -----	MI I KRDNS
YCP3_SYNPY	: -----	MTNQRFKS
SLR0116	: -----	MAVTDLSDLTN

* 60 *	80	
RFLLRW S AVSYKEFAESALEETRKRIVLE B SHIQEKYSSMTGLDGK -		86
----- FDSFLNELHSDITKR ----- GGSF L P E PEGLEE C RSSKSS -		36
----- NKLM LQDL HNNLKRRI - I SHGGKPIEVE NGMSE RF S HKQD -		40
LSKID E RDWI WT PF F NDLV D KL - SVF E IE P PVVS HD F LS KES ITGSR		54
TD PVN E GWSWQPF L EDAIKRL - EGLNVE E YPVPDR FLQRED QTGSK		54
SS LMPTLNPM I QQLALAIAASW - QSLPLK E YQI P EDLG Y VEGRLEG E		56
	B	

*	100	*	120
HY2_ARATH	- - - - T E L Q M L A F K S S K I R L L R S M A D E N - E T Q V F D F A G F		
YCP2_SYNPY	- - - - S V I Q S W I L D V P G F R R W R V T R D A G D S I Q V E L S V A Y		
YHP2_PROMA	- - - - T V I K S W I L D V P G F R R W R V T R D A G D K H Q V L S V A Y		
YHP3_PROMA	R N P V H V T T L T W A A K F E K I K Q V R I A C K G G E S I S V F L I H		
YCP3_SYNPY	S K S I P V T T A T W A C K T E K F R Q V R A A C T S A G S A A S V L I F V I N		
SLR0116	- K - - L V I E N R C Y Q T P Q F E K M H L E L A K V E K G D I L H C V M F		

* 140 *	160 *
ME PE [DTPIFCANF FTSTNVN--] VVFDLNPLHQQLTDQTDYQDKYWN : 165	
[D DYN [DRPLM] CVDLITWEGARQKLWAVLDFQPLVQ --- DKDYLDREYES : 115	
[AYTNDKE[ILCIDIPWFGLKRKLVAVLDFQPLVQ --- EERYFCRYWK : 119	
[LNDVDLPLFFCADEFUTL PNG -- HILALADDLOPAALKL -- DN IHTENVWP : 137	
[PKSTLGLEFFGGDLVTFPAG -- HILALADDLOPAIKT -- DEVHTTHVAD : 137	
[EPELPLEGLEFFGCDIMAGPGG-VSAAIADLSQTOS --- DRQLPAAYOK : 135	
P V P g 1	1D P

Fig. 5



СЕВЕРНОЕ ПОДЪЕМНОЕ

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	180	200	
HY2_ARATH	: KTM----S EYHKV AETFP WG GKLTGESIKDGSPLVMPTR-		
YCP2_SYNPY	: G TK ----E VNQRE PDLNGEE TMR SFD D PNC VPS SWLWICB-		
YHP2_PROMA	: D EQ ----I CKNRI VD FNSQK TMKIYDSNK YDS PHV VLYN -		
YHP3_PROMA	: R EI ----P FRDH W QSLLP SGGEIP KEAEP Y DS PG FID S R L		
YCP3_SYNPY	: R EI ----P IFERW R DQLF Y GGG PIPEEAQ P ES DS PG FID T RL		
SLR0116	: S PAELGQPEFEQQRE LPP WG -----E IRSEY C DN I HL -		

220	*	240	*	260	
FSSSKEKHKAFSAFLEYQALFLENTIQVREEMEPSHVRANCRA					: 244
GGAEQADLSMPKAFSATPKAKWDFHDNAKSIPSTIPPEEVKNL					: 193
GSFDDLQCSNAKILDEETHAWQDNNNNSREYIKIIPSKVETL					: 197
PLSKESDNIISEITRPAFGEWISLIEILHIAKPLKKER-ALKILEG					: 219
PLGEEGDELIIQSIVRPAFNDYEDLLETAASAERTDER-SEVILLG					: 219
PSNVTEEERFVQRVVDLQIHCHQSIVAEPLSEAQ-TLEHRDG					: 208

	*	280	*	300																																					
	S	Y	Dp	G	W	S	LF																																		
HY2_ARATH	Q	H	K	L	T	R	A	Q	D	P	G	H	G	I	L	K	R	L	V	E	A	K	A	K	E	L	R	D	F	L	E	N	G	V	D						
YCP2_SYNPY	:	Q	D	K	Y	D	I	M	S	A	E	R	D	P	A	H	G	L	F	T	S	H	F	G	K	D	:	S	N	R	I	L	H	E	F	L	E	P	A	S	S
YHP2_PROMA	:	H	I	N	E	D	I	X	S	A	E	R	D	P	A	H	G	L	F	K	S	Y	F	Q	T	W	A	D	Q	E	V	R	E	F	L	E	P	H	S	H	
YHP3_PROMA	:	Q	K	A	V	I	N	M	R	S	T	E	D	P	A	R	A	M	L	C	R	F	Y	K	E	N	T	E	D	Y	I	H	K	V	L	E	N	I	--		
YCP3_SYNPY	:	Q	R	K	E	T	D	Y	R	A	E	K	D	P	A	R	G	M	L	T	R	E	H	G	S	E	T	E	A	M	I	H	T	V	I	E	D	L	--		
SLR0116	:	Q	T	H	Y	C	Q	Q	Q	Q	K	N	E	K	T	R	R	V	L	E	K	A	F	G	E	A	A	E	R	I	S	Q	V	I	E	D	V	I	O		

* 320 * 340
ELGTKTFIDYFPEYQTEDGTVDKRSIICKSYETRPWDLTGQFIG 329
SHK----- 236
LTAD----- 241
----- 257
----- 257
----- 248

Fig. 5 cont'd.



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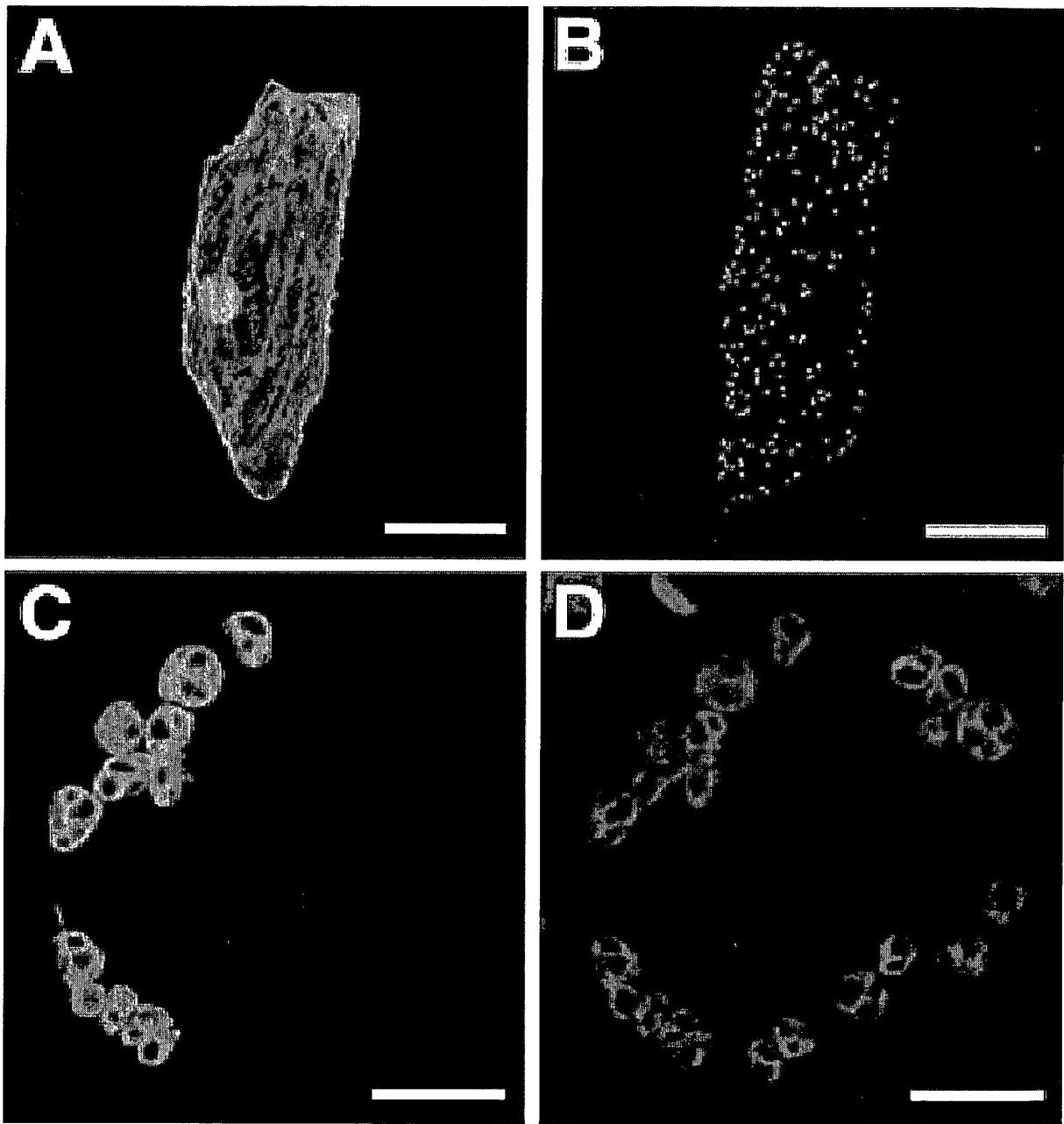


Fig. 6



00 09 03 02 01 00 03 04 05 06 07 08 09 00 01 02 03 04 05 06 07 08 09

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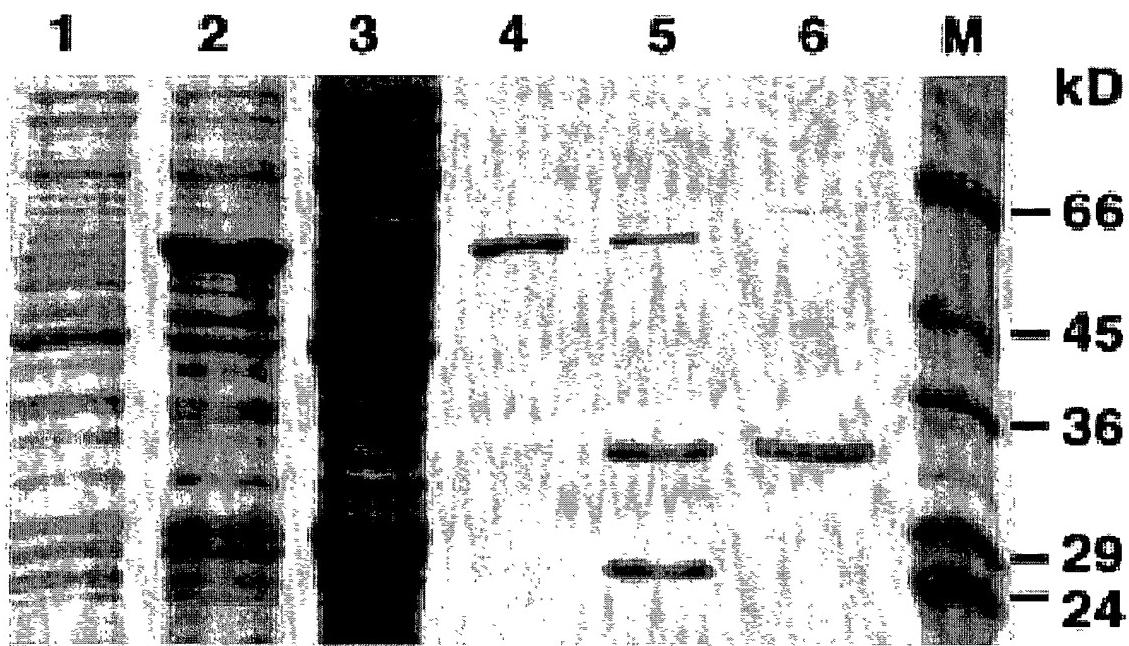


Fig. 7



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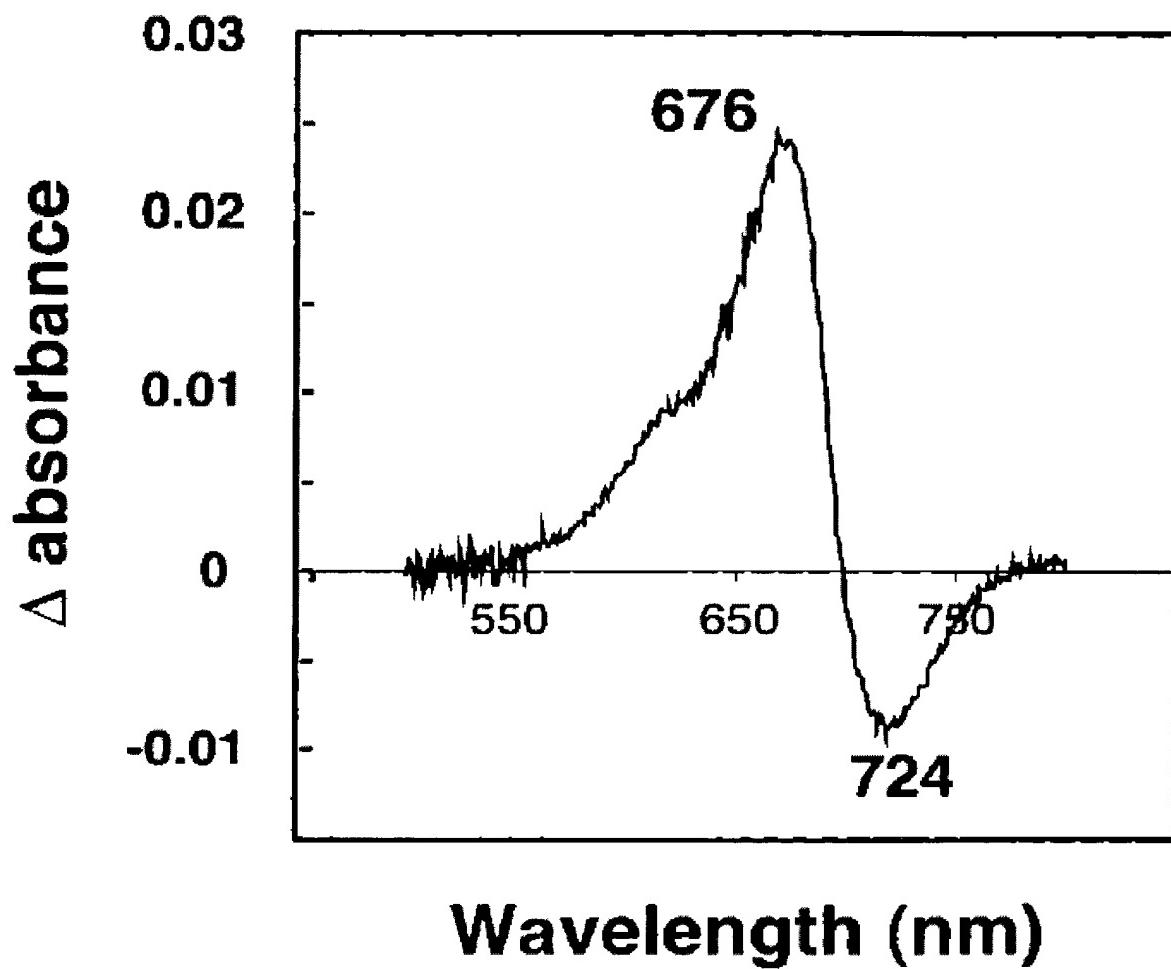


Fig. 8



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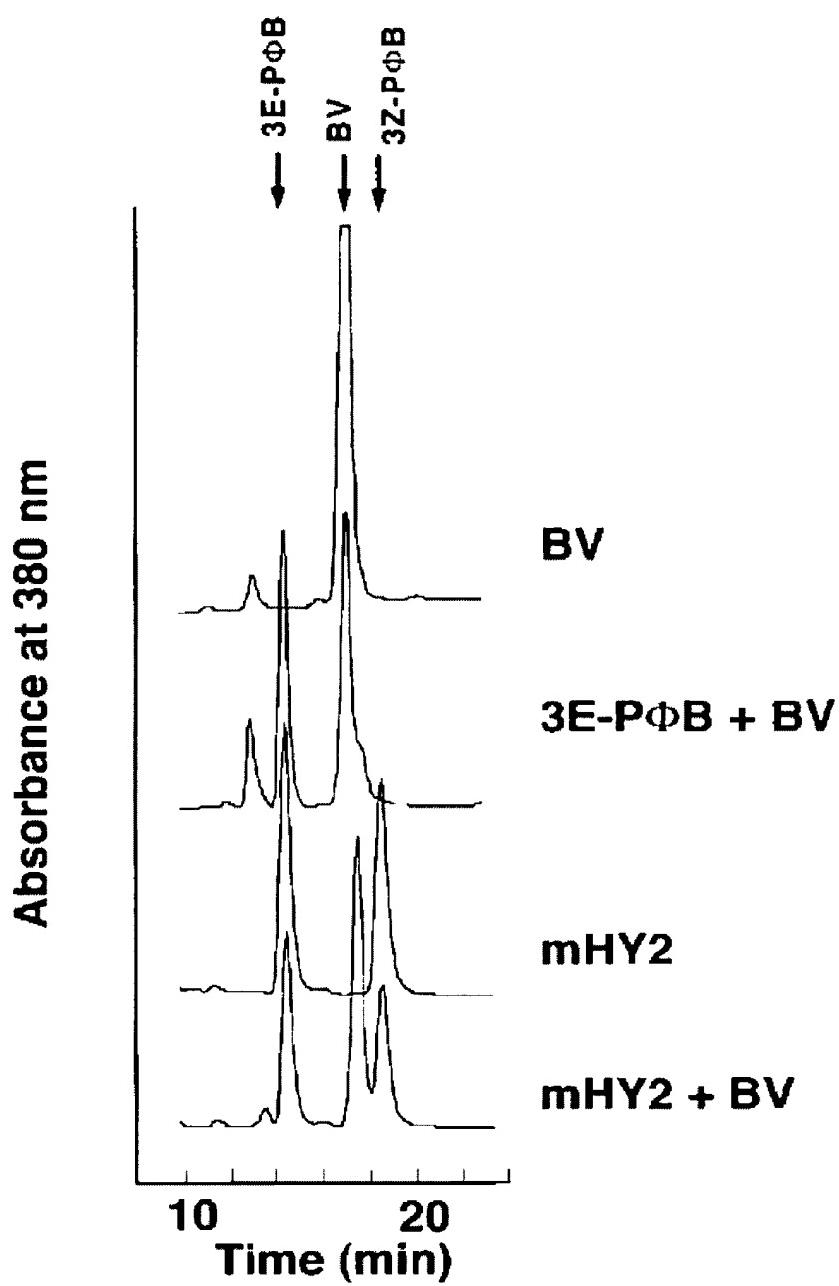


Fig. 9



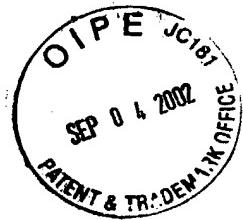
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	20		40
PcyA_ANASP	-----		-----
PcyA_NOSPU	-----		-----
PcyA_SYNY3	-----		-----
PcyA_SYN81	-----		-----
PcyA_PROME	-----		-----
PebA_SYNPY	-----		-----
PebA_SYN81	-----		-----
PebA_PROMA	-----		-----
PebA_PROME	-----		-----
PebB_NOSPU	-----		M LN S Q S P L R N V A
PebB_SYNPY	-----		-----
PebB_SYN81	-----		-----
PebB_PROMA	-----		-----
PebB_PROME	-----		-----
PebB_NOSPU	-----		-----
HY2_ARATH	-----	- M A L S M E F G F S I G S C F K A P N - P P V L I S A	
RCCR_ARATH	M A M I F C N T L Y S S S P S Y L S P L T S K P S R F S K N L R P R A Q F Q S		
RCCK_HORVU	-----		

60	80	
-----MSLTSIPSLREQQHP[RQLADCEEVWHQHLDLS[PAYH[P AEL		: 43
-----MSFTSHPSLREQQHP[RQLADCEEW[HQHLDLS[PAYH[P D E L		: 43
-----MAVTDLSTNSSLMP[TLNPMQQLALAAASWQS-LPLKEYQEPEDL		: 46
-----MQSPPSSESSSTVA[PILPSLAET[RGAWIGLPELKELDADSDF		: 42
-----LNLLSKSLTKTKLIDP[LTLTLLQNIKVQRSKLNDLNCIE[DPKL		: 44
-----FD[DSFLNEHSDIITK-RGGSPLP[P DGL		: 27
-----FD[PFL[EOTGIQA-RGGISVEMPAGL		: 27
-----MNKLQDLHNN[KREIIIS-HGGKRIEMENGM		: 31
-----FESLKNFVKTNTE---DLOGKEEEISK		: 25
TINETCMEAITYFHARVNKSCSYKPFLEFEEKELFQFFDLO5RVIP[PGL		: 64
----MTNQRFKSTD[PVNIEGWSWQPFLEDAIKRLEG-LNVE[PY[PWPDRF		: 44
----MSIDLRASSLDPVQIPGWEWQPFLDEASAA[KP-FNPSPYPIAETF		: 45
----MIIKRDNLSKIDLRDWWT[PFNFDVDKLSV-FETE[PY[PWSHDF		: 44
----MLIQNTIFYSQEWRWAKFIKFISQI[DN-YHCVEHKIASDF		: 40
----MNSERGDT[VYQPFLEDYIAYMRSRLDLE[PYPIPTGF		: 37
KINFTRLRRRKERFLLRVSAVSYKEFAESAETRKR-IVLEPSHLQEKY		: 77
HDDHLRKFMF[PYVSPTRKQIMV[DLMS[TWENRLOS-QLLECNLPPDV		: 90
-----		: -

4

Fig. 10



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100

120

PcyA_ANASP :	GYVEGRLEGEK-----LTIENRCYQTPQFHKMHLAKV
PcyA_NOSPU :	GYVEGRLEGEK-----LTIENRCYQTPQFHKMHLALAN
PcyA_SYN3 :	GYVEGRLEGEK-----LVIENRCYQTPQFHKMHLAKV
PcyA_SYN81 :	SSI EGOLLEGDD-----LLTIRNELLCRGVBKIHLELARL
PcyA_PROME :	SNIISNEEGKE-----BYIENEFYKAKGFEKLHIEVAEPS
PebA_SYNPY :	EECRSSKSS-----SVIQSWLWQVPGFERRWRVTREDA
PebA_SYN81 :	EHNQSQKGS-----STIQSWLWQVPGFERRWRVTREDA
PebA_PROMA :	SERFSHKQD-----TVIKSWLWQVPGFERRWRVTREDA
PebA_PROME :	EFKEHHNKD-----SKYIILKNWIEESQQYKWRITKLDG
PebB_NOSPU :	EFKVSDRGR-----NPATIRSVCYQSQELSKIRTYIDA
PebB_SYNPY :	LQREDQTGSKSK-SIPVTTATWACKTEKFHQVRAACUSA
PebB_SYN81 :	LQKEGSTCSKAK-PVPTTATWACSTDMLHQVRCACUEA
PebB_PROMA :	LSKEISITCSRPN-FVHVTTLTWAAKFEKIHQURLACTKG
PebB_PROME :	SYKESSYGSKKS-KKNINLFTWGATHQKRINFARAVCINS
PebB_NOSPU :	ESNSAVVGKGKN-QEWVTTSYAFQTAKLEQDRAAHVOGE
HY2_ARATH :	SSMTGLDG-----KTEEQMLAEKSSKIRLLRSMAIEN-
RCCE_ARATH :	RNFNNPNGSAEASLHIRSGDKS3PIDFVIGSWIHCKIPT
RCCE_HORVU :	-----MDFLQSSLHCKVPE

9

140

160

180

NMFD	ELHCWJEPERPEWELPMFECIDIVGGR-GQISAAIADLSPVHL---ERTL	: 126
NMFD	ELHCWJEPERPQMNLPMFECIDIVGGR-GQISAAIADLSFQL---ERTL	: 126
KGUD	ELHCWJEPERPEPLVGLP/FECDIVAGP-GGVSAADADLSPTQS---DRQL	: 129
RGD	ELHCWJEPDPREELPIFADIVAGP-AGVSAADADLSPEV---SGTL	: 123
IKSEKILICWJEPDPKMDIPIFGMDIVKVN-ELVSAADADLSPSSSK---NQNL	: 127	
DSTOVENSVAEVDYNEDHPLMWDLWFGARQKLWVAYEDFQELVQ---EKDY	: 109	
DSTOVLNSVAEVDFDLHPLMWDLWFGARQKLWVAYEDFQELVQ---EKDY	: 109	
DKTQVLSVAEVPAYTNDKPILEIDIWFGLKRKLVAVLDFQPEVQ---EERY	: 113	
DKTQVNTVAEPNFKSEFPILEADIWFGTSQKLIAIFPYQPEIQ---EKKY	: 109	
BSAQIFNSWJEPHSNNDPLLGIDFLSGF-KVKNGIVYDFQPEFO---DEDY	: 147	
SAASVLFVINPKSTYGLPFFEGDIDTFP--AGHILADDLOPAIK--TOEVH	: 131	
MAASVLFVINPSCREDFPFPEADIVTLP--NGHILADDLOPVDOK--ADPDH	: 132	
ESIBWMFLLIPLNDYDGPFPEADOFVTLPP--NGHILADDLOPALK--LDNINH	: 131	
PNYSWINFIPIKTSVNIIPFLWDFVSLP--TSHILWDFQPSLK--VENQF	: 127	
NSDQVNFVIEPHLNWDFPFPEADIVTLP--GGHILADDMQPEFR--DT SAY	: 124	
ETMOVFDAGEMEPEYDTPTFCANFFTST--MVNVWYCDLNPLHQLTDQTDY	: 159	
VSNITCISGELNSSTKAPNEVVELIOSS-SKSLVLLDDLPHRKDLVLNPDY	: 181	
-AIDIITSLFINLNASTDAPEHEIMEFIQGS-PTSMWVLLDLLERKDLALHPEY	: 66	

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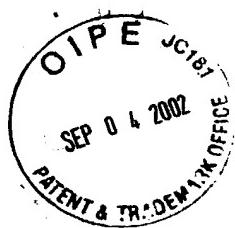
P

P

G 1 4

D P

Fig. 10 cont'd.



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	200	220
PcyA_ANAS P	PESYNSALTSENT---LNF SQP REL P WGN I ---	ESDF
PcyA_NOSPU	PES YTT ALAQPPV --- LNF SQP REL P WGN I ---	ESDF
PcyA_GNY3	PAAYQKSLAEDGQ --- PE FEO QREL PFWGEI ---	PSBY
PcyA_SYNRI	PSG IET ALAGTPS --- PA FRQ V RD L PGWGT I ---	PS PH
PcyA_PROME	-- KYDHL LSH DOK --- SVF KSKRE I PIWGNI ---	ESKN
PebA_SYNPY	LDRYFSGLKEENQRF PDL NGEET MRS FEPNQ ---	ESSW
PebA_SYNB1	LDRHFDGLKDENARF PDL NGEET MRS FEPNQ ---	ESSW
PebA_PRONA	FCRYYKDLQIEKNRPVDFNSQKTMKIYDSNK ---	ESPW
PebA_PROME	LOKYCS SLDPEKNOVSVDNHKMKN I YDSKK ---	ESPW
PebA_NOSPU	QNKYIAPIKYDHNKY PDL AQNLEMKFYDANO ---	ESKY
PebB_SYNPY	TTHVWDRLLIPF ERWRDQL PYGGPIPEEAQPF ---	ESP G
PebB_SYNB1	TQPVWERLMPFFERWQAE L P DGG PIPEEAQPF ---	ESPA
PebB_PRONA	TENVWPRLLIPFHDHWQSL L P SGGEI PKEAEPV ---	ESP G
PebB_PROME	NSELLEQIIKIKKSCHSSL PVA E KMSEIVAKS ---	ESP G
PebB_NOSPU	QAKYTEPILPUFHAKQHLSWGGDFPEEAQPF ---	ESPA
HY2_ARATH	QDKYVWKIMS YHKYAETFPWGGKL TGESIKE ---	ESPL
ROCR_ARATH	LKEYYQDTALDSHRQS LLKLPDVNDYVS PSLFVRSA ---	ESPT
RCCR_HORVU	IEKY YEDTEVKDQRKI IEQLPQAEPYLS PSLFVRSA ---	ESPT

4

ES

	240	260	
C'DW'R P	-SSPSEE EAMFIGRV RIEI QWHCQGAI AA -- SPVSAEOK	: 199	
C'DW'R P	-GSPSEE EAMFLSRV RIEI QUDI HCMQAI AS -- HPVSV EQV	: 199	
C'DW'R P	-SNVTE EERFVQRV VIDEI QI HCHQS IVA -- EPESEAQT	: 202	
MC'DW'R P	-DGAEEK EVLFRSRV EEEV UPI LRTAVI QTACEP A ST	: 198	
MF'FASL	-KNESEKNAFCKI VDNMISMLIQLSQST -- SPDSDYEI	: 198	
IL'DW'R G	-CAEQADLS EPKAFSAEIKAKNDLH DMA -- KSI PSTDIP	: 186	
IL'DW'R G	-GSEBADRS EPKAFSAEIKAKNGLHDEA -- SKEPSSIS	: 186	
M'DW'YNG	-SFDDQLQCSEAKI LDEEULHANQVDNNN -- SREYIKII	: 190	
M'DW'ORG	-NKLNLDRDUNNI FCSFVSNM TTIN KIH -- ONNOFID	: 185	
L'DW'ANT	-DAETVSTRWFEAFQDYLNLWQMLADA -- QA BHD PED	: 224	
IF'DW'TRLPLGE	-EGDELIQSIVEPAFNEYLDEELELAASA -- ERWTDERS	: 213	
IF'DW'TRIPLGE	-EGDELIERV EFAPIEYIQLLENLVAEA -- EPVSDDRA	: 214	
IF'DW'SRLPLSK	-ESDNII SEI ERFAPCEYLSLHELLHIA -- KPLKKE RA	: 213	
IL'DW'SRLAKHQ	-DSDNLIENQLEYDSFKEYINLNUKTLFES -- EEVGHGLQ	: 209	
IF'DW'TRP	-QETAVVETQWFAAFKDVILKAMLD FVEQA -- EA VTD SQN	: 202	
M'DW'RF	-SSSKEKHKAI FSAF LEVYQA MENTIQV -- RE EME PSH	: 237	
A'SMLKIDAE	-EDKLESILRDHOSPAAKEV L E VV L E RCVKEEEKIVV GEE	: 271	
A'WSEFT IDCGKGCEGTLEEIVHGHMASVVKGILQI W DTC ASD -- ASEMEE EG	: 155		

4

Fig. 10 cont'd.



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	2 8 0	*	3 0 0	*
PcyA_ANASP :	GGI[REDACTED]A-G[REDACTED]HNYC[REDACTED]SKOOON[REDACTED]	D[REDACTED]KTRRVL[EKA[REDACTED]FGVDDAEN[REDACTED]	HMTT	
PcyA_NOSPU :	TQ[REDACTED]A-G[REDACTED]HNYC[REDACTED]TKQQON[REDACTED]	D[REDACTED]KIRRVL[EKA[REDACTED]GPVVAEN[REDACTED]	HMTT	
PcyA_SYN3 :	LEH[REDACTED]RQ-G[REDACTED]IHYC[REDACTED]QQQQKN[REDACTED]	D[REDACTED]KTRRVL[EKA[REDACTED]GEADAER[REDACTED]	MMSQ	
PcyA_SYN81 :	I[REDACTED]RYE-G[REDACTED]LSY[REDACTED]LQQKRN[REDACTED]	D[REDACTED]KTRRVL[EKA[REDACTED]DASMAADRMISE		
PcyA_PROME :	I[REDACTED]EERINY[REDACTED]KNYC[REDACTED]VQQMKN[REDACTED]	E[REDACTED]KTS[REDACTED]LULLKYF[REDACTED]DKVVM[REDACTED]	MIKK	
PebA_SYNPY :	P[REDACTED]EEW[REDACTED]KNULD[REDACTED]DKYD[REDACTED]IYSAER[REDACTED]	D[REDACTED]PAHGLFT[REDACTED]SHFGKDOSNR[REDACTED]	ELHE	
PebA_SYN81 :	P[REDACTED]GDWERL[REDACTED]QNA[REDACTED]DVYS[REDACTED]AER[REDACTED]	D[REDACTED]PAHGLFT[REDACTED]SHFGKEDOSDR[REDACTED]	ELHE	
PebA_PRMMA :	P[REDACTED]SKW[REDACTED]EQQLHINYD[REDACTED]IYSAER[REDACTED]	D[REDACTED]PAHGLFKSYF[REDACTED]GOT[REDACTED]DO[REDACTED]	EWRE	
PebA_PROME :	L[REDACTED]E[REDACTED]QKNN[REDACTED]IDYD[REDACTED]KYSABE[REDACTED]	D[REDACTED]PADKLFKTF[REDACTED]GET[REDACTED]TEN[REDACTED]	ELINN	
PebA_NOSPU :	I[REDACTED]QR[REDACTED]IVKA[REDACTED]OKDYD[REDACTED]QYSADR[REDACTED]	D[REDACTED]PASGLFSSYFGHE[REDACTED]AARR[REDACTED]	ELRE	
PebB_SYNPY :	E[REDACTED]VL[REDACTED]DQ[REDACTED]GURKYTDYRAEK[REDACTED]	D[REDACTED]PARGM[REDACTED]LTFRHGS[REDACTED]EMTEA[REDACTED]	MIHT	
PebB_SYN81 :	E[REDACTED]LL[REDACTED]ES-G[REDACTED]KRYTA[REDACTED]YRAEK[REDACTED]	D[REDACTED]PARGM[REDACTED]LTFYG[REDACTED]GSE[REDACTED]NTES[REDACTED]	MIHG	
PebB_PRMMA :	L[REDACTED]K[REDACTED]IPE-G[REDACTED]KAYI[REDACTED]NYRSTK[REDACTED]	D[REDACTED]PARAMLCRFY[REDACTED]GKEMTED[REDACTED]	MIHK	
PebB_PROME :	Q[REDACTED]EL[REDACTED]EN-G[REDACTED]NDYLNYRRDN[REDACTED]	D[REDACTED]PARPM[REDACTED]S[REDACTED]LFECKD[REDACTED]TBSLINK		
PebB_NOSPU :	L[REDACTED]VA[REDACTED]IKQA[REDACTED]DLRYLRYRAEK[REDACTED]	D[REDACTED]PARGM[REDACTED]KRFY[REDACTED]GAED[REDACTED]TRE[REDACTED]	MIHG	
HY2_ARATH :	V[REDACTED]RANCEA[REDACTED]DKYLTWRAQKD[REDACTED]	D[REDACTED]PGHGLL[REDACTED]KRLVGEAKAKELLRD		
RCCR_ARATH :	E[REDACTED]RHELER[REDACTED]RDKSFRRKSIE[REDACTED]	D[REDACTED]DLDLQF[REDACTED]PRMF[REDACTED]GEE[REDACTED]VS[REDACTED]	RCCR	
RCCR_HORVU :	E[REDACTED]ERE[REDACTED]MVK[REDACTED]RDR[REDACTED]TVRSKSIE[REDACTED]	D[REDACTED]VDLTANL[REDACTED]PRMF[REDACTED]GPDSGR[REDACTED]	RIIRE	
	Q Y	1	4	3G
				4

	3 2 0	*	3 4 0	*	3 6 0	
VLFOLPE-----						: 245
VLFOLPT-----						: 245
VLFODV1Q-----						: 248
LLFDDPLPPG-----						: 247
VLFDF-----						: 243
FLFPASSSHK-----						: 236
FLFPASQPA-----						: 235
FLFPHSHTAD-----						: 241
FLFELNHNPLK-----						: 236
FLFEDAVPLAVSASKR-----						: 280
VLFOL-----						: 257
VLFOLEDAA-----						: 262
VLFENI-----						: 257
VLFETNKVL-----						: 257
FLFOLERKLTVVK-----						: 255
FLFNGVOELGTRTFIDYFPEYQTEBGTVSDKRSITIGKSYETRPWDLTGQFIG						: 329
TRKAFGVL-----						: 319
TRKAFGVQEG-----						: 205
LF						

Fig. 10 cont'd.



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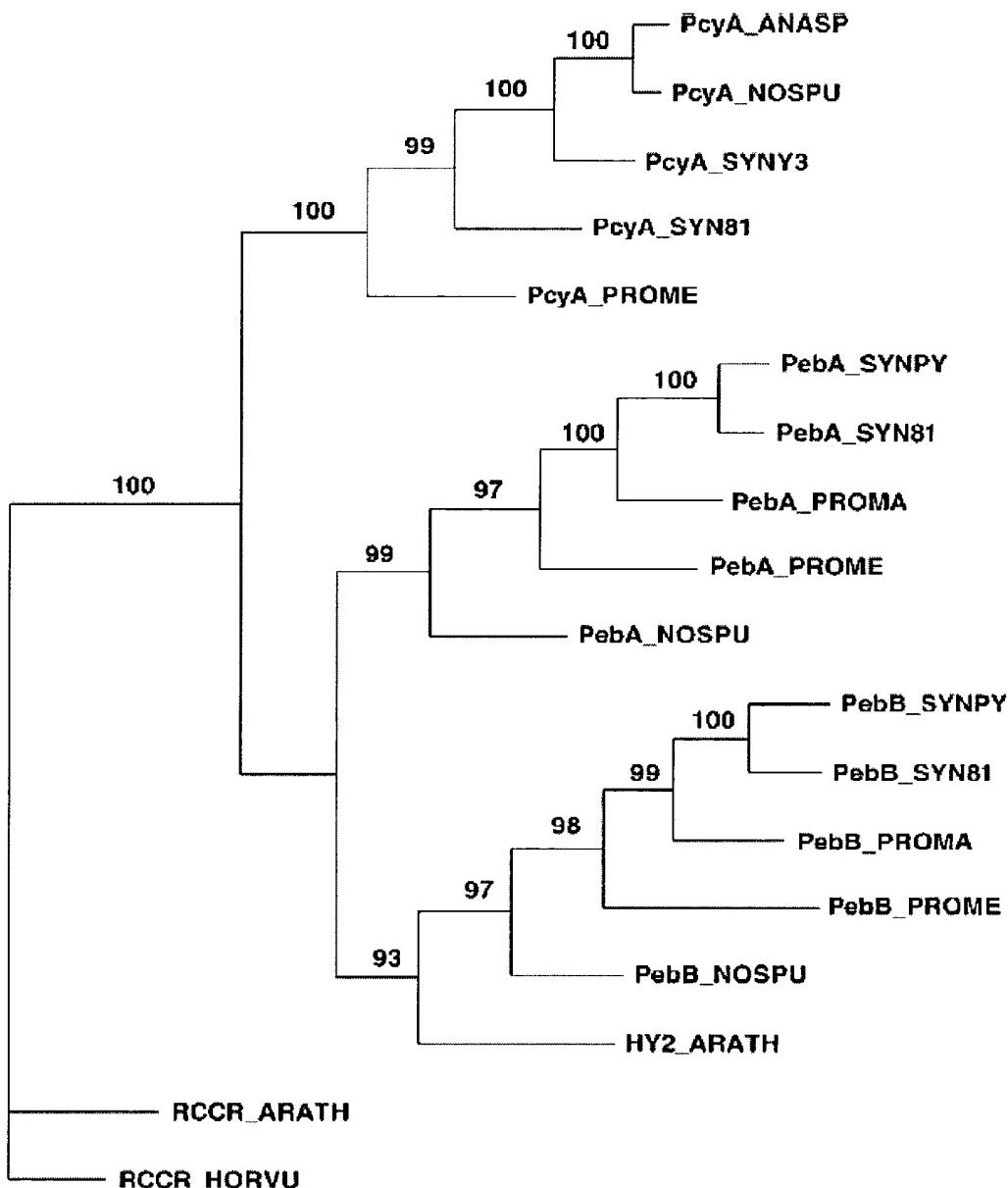
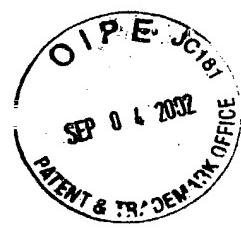


Fig. 11



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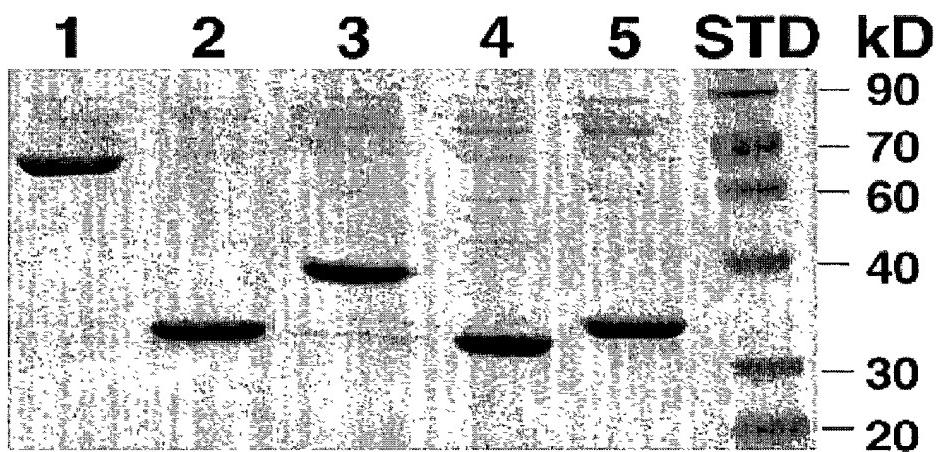
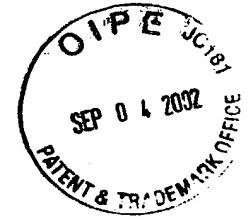


Fig. 12



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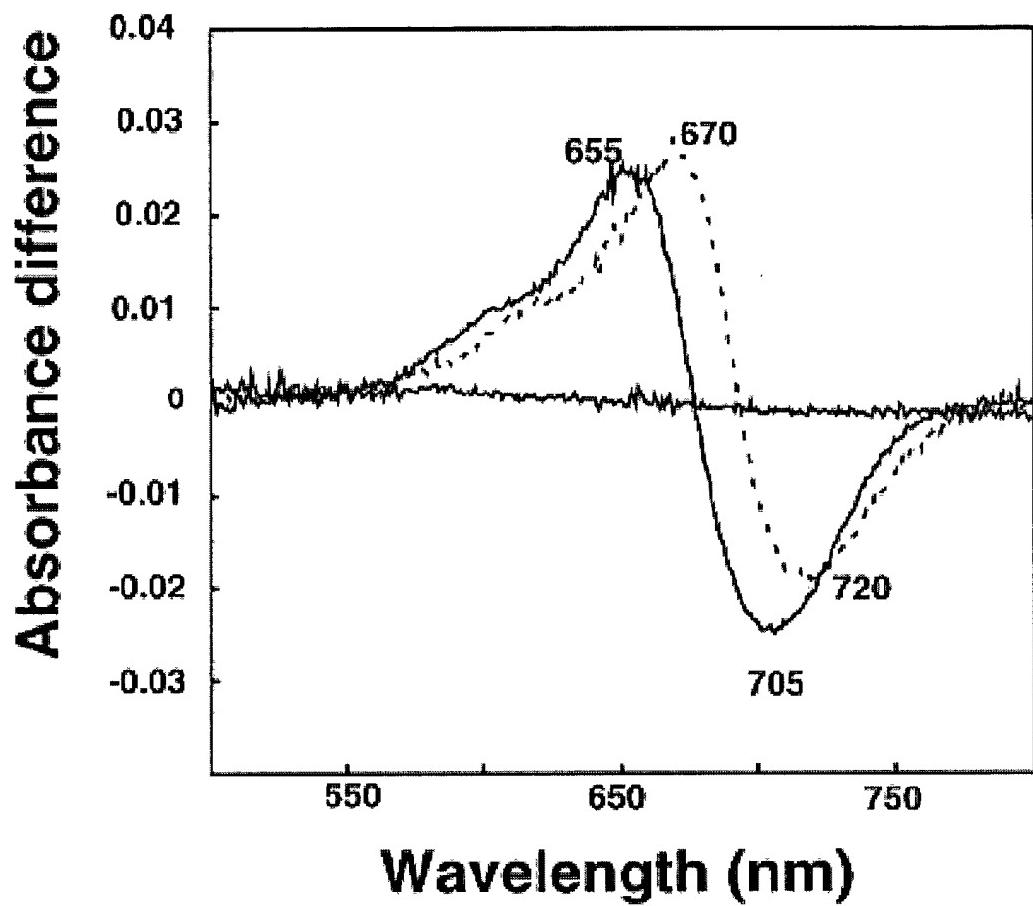


Fig. 13A



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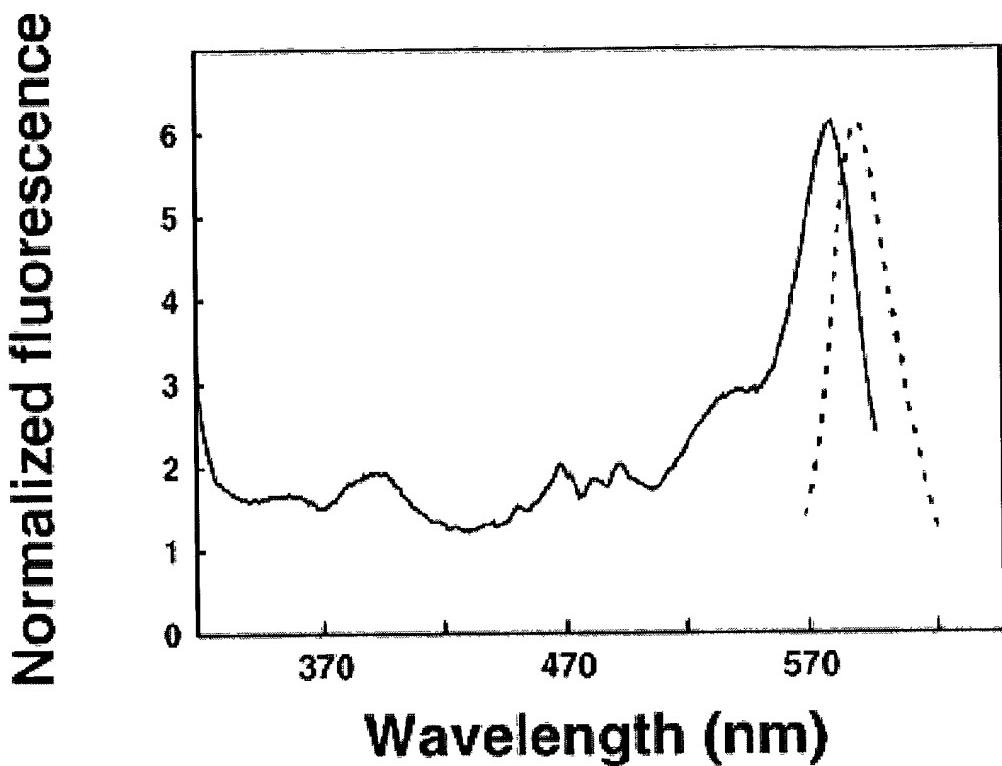


Fig. 13B



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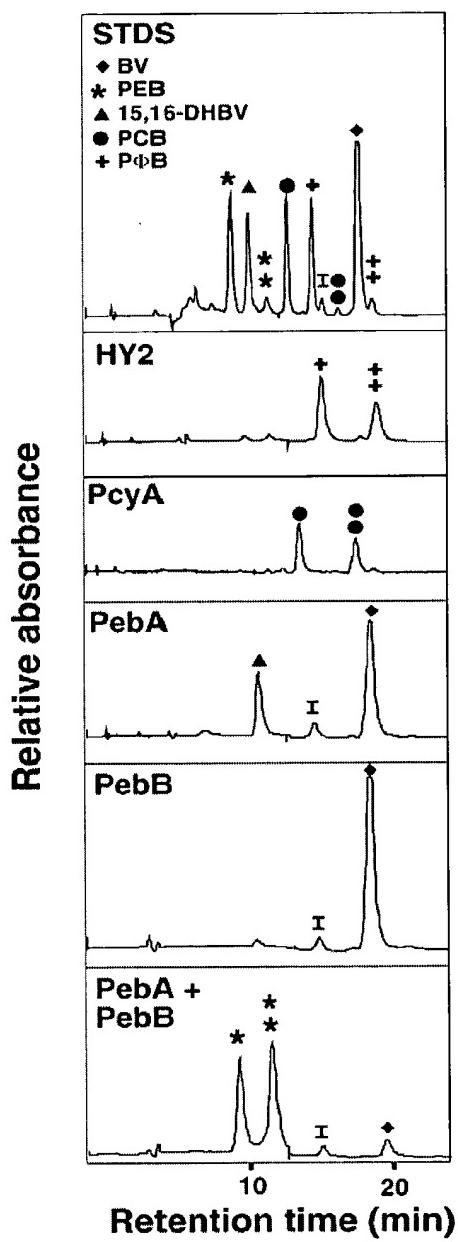


Fig. 14



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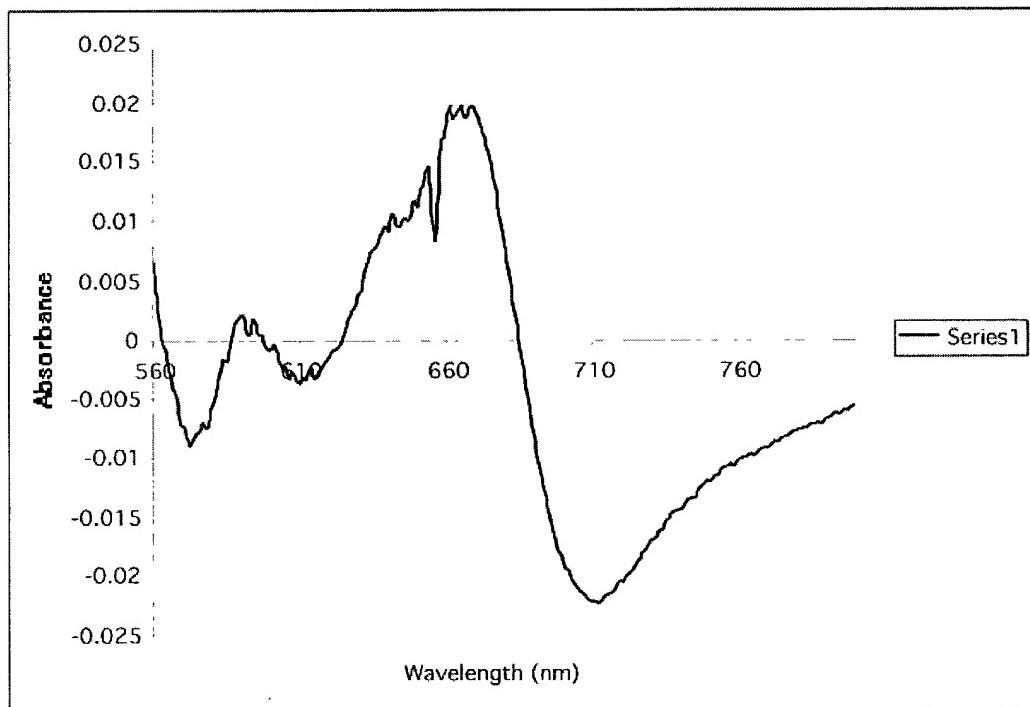


Fig. 15



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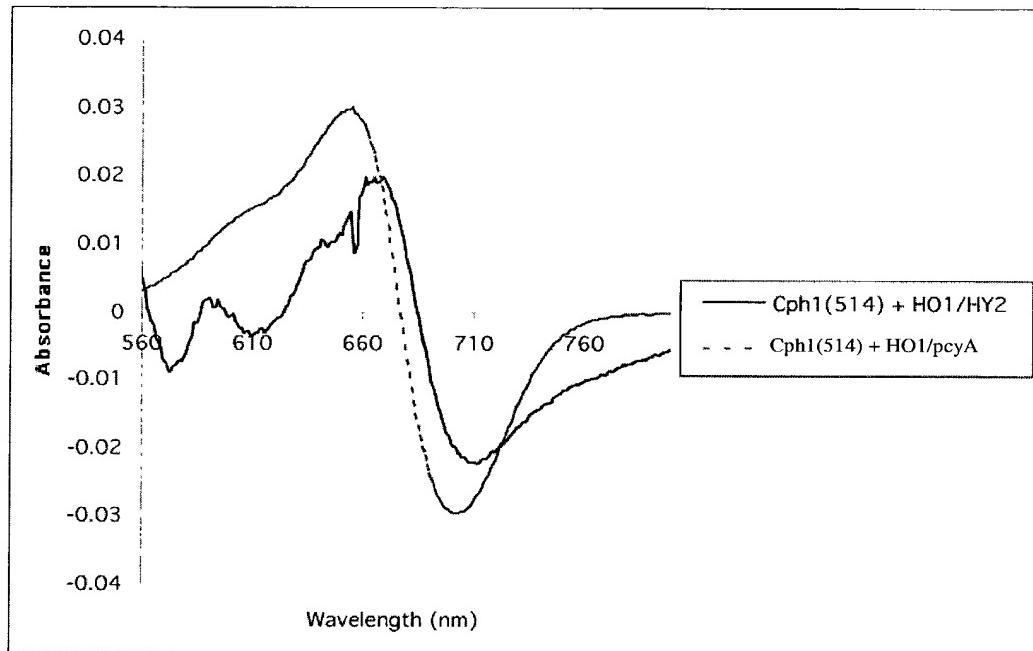


Fig. 16